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#### SEQUENCE LISTING

<110> The United States of America as Represented by the Secretary of the Department of Health and Human Services, Centers for Disease Control and Prevention

Liu, Hsi Steiner, Bret Berta, Rodes

- <120> COMPOSITIONS AND METHODS FOR DETECTING TREPONEMA PALLIDUM
- <130> 6395-61666
- <150> PCT/US00/16425
- <151> 2000-06-14
- <150> US 60/138,981
- <151> 1999-06-14
- <160> 26
- <170> PatentIn version 3.1
- <210> 1
- <211> 2945
- <212> DNA
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Leu Ala Ser Leu Pro Ser Arg Val Pro Ala Arg Pro Ala Gln Arg Asp 85 90 95

Pro Leu Ser Ser Pro Pro Ala Gly His Thr Val Pro Glu Tyr Arg Asp 100 105 110

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Val Val Pro Glu Glu Gln Lys Gly Arg Ala His Pro Gln Val Ile Pro 450 460

Glu Gly Ala Pro Arg Gly Leu Gln Pro Gly Glu Tyr Tyr Val Gln Ile 465 470 475 480

Ala Val Phe His Asp Ala Ile Gln Val Gln Ser Ile Val His Arg Tyr 485 490 495

Gly Val Glu Tyr Pro Ile Ala Val Glu Gln Asp Ile His Glu Gly Lys 500 505 510

Val Arg Phe Thr Val Cys Val Gly Pro Val Gln Lys Asp Glu Arg Gly 515 520 525

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Lys Lys Ala Arg 545

<210> 21

<211> 1047

<212> DNA

<213> Treponema pallidum

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agc aa Ser As												96
gca gg Ala Gl												144
cag ct Gln Le 50	u Gly											192
ttg gg Leu Gl 65												240
ctt gc Leu Al												288
cct ct Pro Le												336
acg gt Thr Va		Phe										384
gtg ga Val Gl 13	u Asp											432
ggg ga Gly Gl 145												480
gag cg Glu Ar												528
gag cc Glu Pr												576
ccg aa Pro Ly												624

195	200	205	
gtc gct tct cag cat Val Ala Ser Gln His 210			
gct ccc aat cag ttt Ala Pro Asn Gln Phe 225			
cct gac cta tcc gag Pro Asp Leu Ser Glu 245	Ser Glu Ile Val		_
cgt gcg cat ccc cag Arg Ala His Pro Gln 260		Gly Ala Pro Arg G	
cct ggt gaa tac tac Pro Gly Glu Tyr Tyr 275			<del>-</del>
gtg cag agc att gtc Val Gln Ser Ile Val 290			
gag cag gac atc cat Glu Gln Asp Ile His 305	, ,, ,,,	2	2 2 22
cct gtc caa aaa gac Pro Val Gln Lys Asp 325	Glu Arg Gly Ala		
ttt gga ttc aag gac Phe Gly Phe Lys Asp 340	_		1047
<210> 22 <211> 348 <212> PRT <213> Treponema pa	llidum		
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<400> 22			
Met Phe Val Arg Ser 1 5	Asp Met Phe Pro	Lys Asn Thr Ala V 10	al Glu Ile 15
Ser Asn Leu Glu Lys 20	Asn Ala Lys Ala 25		le Gly His O
Ala Gly Ile Pro Gly 35	Leu Leu Val Ser 40	Leu Ala Pro Ala A	ala Ala Ala

- Gln Leu Gly Ile Gly Val Tyr Gln Ala Val Arg Val Arg Thr 50 . 55 60
- Leu Gly Thr Val Arg Gly Gly Ser Gln Thr Ser Gln Asp Gly Leu Ser 65 70 75 80
- Leu Ala Ser Leu Pro Ser Arg Val Pro Ala Arg Pro Ala Gln Arg Asp 85 90 95
- Pro Leu Ser Ser Pro Pro Ala Gly His Thr Val Pro Glu Tyr Arg Asp 100 105 110
- Thr Val Ile Phe Asp Asp Pro Arg Leu Val Ser Pro Leu Ser Arg Glu 115 120 125
- Val Glu Asp Val Pro Lys Val Val Glu Pro Ala Ser Glu Arg Glu Gly 130 135 140
- Gly Glu Arg Glu Val Glu Asp Val Pro Lys Val Val Glu Pro Ala Ser 145 150 155 160
- Glu Arg Glu Gly Glu Arg Glu Val Glu Asp Val Pro Lys Val Val 165 170 175
- Glu Pro Ala Ser Glu Arg Glu Gly Gly Glu Arg Glu Val Glu Asp Val 180 185 190
- Pro Lys Val Val Glu Pro Ala Ser Glu Arg Glu Gly Gly Glu Arg Glu 195 200 205
- Val Ala Ser Gln His Thr Lys Gln Pro Ser His Ser Val Ser Asn Ser 210 215 220
- Ala Pro Asn Gln Phe Arg Asn Pro Glu Gly Glu Leu Pro Phe Thr Leu 225 230 235 240
- Pro Asp Leu Ser Glu Ser Glu Ile Val Val Pro Glu Glu Gln Lys Gly
  245 250 255
- Arg Ala His Pro Gln Val Ile Pro Glu Gly Ala Pro Arg Gly Leu Gln 260 265 270
- Pro Gly Glu Tyr Tyr Val Gln Ile Ala Val Phe His Asp Ala Ile Gln 275 280 285

290 295 300	
Glu Gln Asp Ile His Glu Gly Lys Val Arg Phe Thr Val Cys Val Gly 305 310 315 320	
Pro Val Gln Lys Asp Glu Arg Gly Ala Val Leu Glu Asn Phe Gln Arg 325 330 335	
Phe Gly Phe Lys Asp Ala Phe Leu Lys Lys Ala Arg 340 345	
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atg ttt gtg cgc agt gac atg ttc ccc aaa aac act gct gtt gaa att 4 Met Phe Val Arg Ser Asp Met Phe Pro Lys Asn Thr Ala Val Glu Ile 1 5 10 15	18
atg ttt gtg cgc agt gac atg ttc ccc aaa aac act gct gtt gaa att  Met Phe Val Arg Ser Asp Met Phe Pro Lys Asn Thr Ala Val Glu Ile  1 5 10 15  agc aac tta gaa aag aat gcc aag gct cag gca gtg gtt att ggg cac  Ser Asn Leu Glu Lys Asn Ala Lys Ala Gln Ala Val Val Ile Gly His	96
atg ttt gtg cgc agt gac atg ttc ccc aaa aac act gct gtt gaa att  Met Phe Val Arg Ser Asp Met Phe Pro Lys Asn Thr Ala Val Glu Ile  1	96
atg ttt gtg cgc agt gac atg ttc ccc aaa aac act gct gtt gaa att  Met Phe Val Arg Ser Asp Met Phe Pro Lys Asn Thr Ala Val Glu Ile  1	)6  4
atg ttt gtg cgc agt gac atg ttc ccc aaa aac act gct gtt gaa att  Met Phe Val Arg Ser Asp Met Phe Pro Lys Asn Thr Ala Val Glu Ile  1	96

								ttg Leu								384
								gag Glu								432
								ccg Pro								480
								gtg Val								528
								ggg Gly 185								576
								gag Glu								624
								gag Glu								672
ggg Gly 225	gag Glu	cgt Arg	gag Glu	gtg Val	gag Glu 230	gac Asp	gtg Val	ccg Pro	aag Lys	gta Val 235	gtg Val	gag Glu	ccg Pro	gcc Ala	tct Ser 240	720
								gtg Val								768
								ggg Gly 265								816
								gag Glu								864
								cca Pro								912
								gag Glu								960
								gtg Val								1008
								gag Glu 345								1056
cct	ggt	gaa	tac	tac	gta	cag	att	gca	gtc	ttt	cat	gac	gct	atc	cag	1104

355 360 365	
gtg cag agc att gtc cac cgt tac ggg gta gaa tac ccc atc gca gtg Val Gln Ser Ile Val His Arg Tyr Gly Val Glu Tyr Pro Ile Ala Val 370 375 380	1152
gag cag gac atc cat gaa ggt aag gtg cgt ttc acc gta tgc ggt Glu Gln Asp Ile His Glu Gly Lys Val Arg Phe Thr Val Cys Val Gly 385 390 395 400	1200
cct gtc caa aaa gac gaa cgc ggc gcg gta cta gag aac ttc caa agg Pro Val Gln Lys Asp Glu Arg Gly Ala Val Leu Glu Asn Phe Gln Arg 405 410 415	1248
ttt gga ttc aag gac gcc ttt ctg aaa aag gcg cga tga Phe Gly Phe Lys Asp Ala Phe Leu Lys Lys Ala Arg 420 425	1287
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20 25 30  Ala Gly Ile Pro Gly Leu Leu Val Ser Leu Ala Pro Ala Ala Ala Ala	
Ala Gly Ile Pro Gly Leu Leu Val Ser Leu Ala Pro Ala Ala Ala Ala Ala 35  Gln Leu Gly Ile Gly Val Tyr Gln Ala Val Arg Val Arg Val Arg Thr	
Ala Gly Ile Pro Gly Leu Leu Val Ser Leu Ala Pro Ala Ala Ala Ala Ala Ala 35  Gln Leu Gly Ile Gly Val Tyr Gln Ala Val Arg Val Arg Val Arg Thr 50  Leu Gly Thr Val Arg Gly Gly Ser Gln Thr Ser Gln Asp Gly Leu Ser	
Ala Gly Ile Pro Gly Leu Leu Val Ser Leu Ala Pro Ala Ala Ala Ala Ala Gln Leu Gly Ile Gly Val Tyr Gln Ala Val Arg Val Arg Val Arg Thr Gly Thr Val Arg Gly Gly Ser Gln Thr Ser Gln Asp Gly Leu Ser 70 Ty 80 Leu Ala Ser Leu Pro Ser Arg Val Pro Ala Arg Pro Ala Gln Arg Asp	

Val	Glu 130	Asp	Val	Pro	Lys	Val 135	Val	Glu	Pro	Ala	Ser 140	Glu	Arg	Glu	Gly
Gly 145	Glu	Arg	Glu	Val	Glu 150	Asp	Val	Pro	Lys	Val 155	Val	Glu	Pro	Ala	Ser 160
Glu	Arg	Glu	Gly	Gly 165	Glu	Arg	Glu	Val	Glu 170	Asp	Val	Pro	Lys	Val 175	Val
Glu	Pro	Ala	Ser 180	Glu	Arg	Glu	Gly	Gly 185	Glu	Arg	Glu	Val	Glu 190	Asp	Val
Pro	Lys	Val 195	Val	Glu	Pro	Ala	Ser 200	Glu	Arg	Glų	Gly	Gly 205	Glu	Arg	Glu
Val	Glu 210	Азр	Val	Pro	Lys	Va-1 215	Val	Glu	Pro	Ala	Ser 220	Glu	Arg	Glu	Gły
Gly 225	Glu	Arg	Glu	Val	Glu 230	Asp	Val	Pro	Lys	Val 235	Val	Glu	Pro	Ala	Ser 240
Glu	Arg	Glu	Gly	Gly 245	Glu	Arg	Glu	Val	Glu 250	Asp	Val	Pro	Lys	Val 255	Val
Glu	Pro	Ala	Ser 260	Glu	Arg	Glu	Gly	Gly 265	Glu	Arg	Gľu	Val	Glu 270	Asp	Val
Pro	Lys	Val 275	Val	Glu	Pro	Ala	Ser 280	Glu	Arg	Glu	Gly	Gly 285	Glu	Arg	Glu
Val	Ala 290	Ser	Gln	His	Thr	Lys 295	Gln	Pro	Ser	His	Ser 300	Val	Ser	Asn	Ser
Ala 305	Pro	Asn	Gln	Phe	Arg 310	Asn	Pro	Glu	Gly	Glu 315	Leu	Pro	Phe	Thr	Leu 320
Pro	Asp	Leu	Ser	Glu 325	Ser	Glu	Ile	Val	Val 330	Pro	Glu	Glu	Gln	Lys 335	Gly
Arg	Ala	His	Pro 340	Gln	Val	Ile	Pro	Glu 345	Gly	Ala	Pro	Arg	Gly 350	Leu	Gln
Pro	Gly	Glu 355	Tyr	Tyr	Val	Gln	Ile 360	Ala	Val	Phe	His	Asp 365	Ala	Ile	Gln

96



Val Gln Ser Ile Val His Arg Tyr Gly Val Glu Tyr Pro Ile Ala Val 370  $$\rm 375$$ 

Glu Gln Asp Ile His Glu Gly Lys Val Arg Phe Thr Val Cys Val Gly 385 390 395 400

Pro Val Gln Lys Asp Glu Arg Gly Ala Val Leu Glu Asn Phe Gln Arg
405 410 415

Phe Gly Phe Lys Asp Ala Phe Leu Lys Lys Ala Arg
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<211> 1182

<212> DNA

<213> Treponema pallidum

<220>

<221> CDS

<222> (1)..(1182)

<223>

<220>

<221> misc feature

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Met	Phe	Val	Arg	Ser	Asp	Met	Phe	Pro	Lys	Asn	Thr	Ala	Val	Glu	Ile	
1				5					1.0					15		

agc aac tta gaa aag aat gcc aag gct cag gca gtg gtt att ggg cac Ser Asn Leu Glu Lys Asn Ala Lys Ala Gln Ala Val Val Ile Gly His 20 25 30

gca ggg atc ccc ggt ctt cta gtt agc ctt gca ccc gct gct gca gca 144
Ala Gly Ile Pro Gly Leu Leu Val Ser Leu Ala Pro Ala Ala Ala Ala
35 40 45

cag ctt ggg att ggc gta tac caa gct gtg cgt gta cgc gta cgt acc 192
Gln Leu Gly Ile Gly Val Tyr Gln Ala Val Arg Val Arg Val Arg Thr
50 55 60

ttg ggt acc gtg cgc ggt ggg tct caa aca agt cag gac gga ctg tcc
Leu Gly Thr Val Arg Gly Gly Ser Gln Thr Ser Gln Asp Gly Leu Ser
70 75 80

ctt gca tct ttg ccg tcc cgt gtg cct gcg cgc ccc gcg cag cgt gat
Leu Ala Ser Leu Pro Ser Arg Val Pro Ala Arg Pro Ala Gln Arg Asp
85 90 95

cet etg tea tee eeg eeg gea ggt eac act gta eeg gaa tat ege gat
Pro Leu Ser Ser Pro Pro Ala Gly His Thr Val Pro Glu Tyr Arg Asp
100 105 110

acg Thr	gtt Val	att Ile 115	ttc Phe	gat Asp	gac Asp	ccg Pro	cgt Arg 120	ttg Leu	gtt Val	tcc Ser	cct Pro	ttg Leu 125	tct Ser	cgt Arg	gag Glu	384
gga Gly	ggg Gly 130	gag Glu	cgt Arg	gag Glu	gtg Val	gag Glu 135	gac Asp	gtg Val	ccg Pro	aag Lys	gta Val 140	gtg Val	gag Glu	ccg Pro	gcc Ala	432
					ggg Gly 150											480
					gag Glu											528
					gag Glu											576
					ccg Pro											624
					gtg Val											672
					ggg Gly 230											720
					gag Glu											768
					cca Pro											816
					gag Glu										cta Leu	. 864
					gtg Val											912
					gag Glu 310											960
					gca Ala										Ser	1008
					ggg Gly											1056

## accarace arater.

				,											
atc ca Ile Hi		Gly													1104
aaa ga Lys As 37	p Glu														1152
aag ga Lys As 385								tga							1182
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Ser As	n Leu	Glu 20	Lys	Asn	Ala	Lys	Ala 25	Gln	Ala	Val	Val	Ile 30	Gly	His	
Ala Gl	y Ile 35	Pro	Gly	Leu	Leu	Val 40	Ser	Leu	Ala	Pro	Ala 45	Ala	Ala	Ala	
Gln Le 50		Ile	Gly	Val	Tyr 55	Gln	Ala	Val	Arg	Val 60	Arg	Val	Arg	Thr	
Leu Gl 65	y Thr	Val	Arg	Gly 70	Gly	Ser	Gln	Thr	Ser 75	Gln	Asp	Gly	Leu	Ser 80	
Leu Al	a Ser	Leu	Pro 85	Ser	Arg	Val	Pro	Ala 90	Arg	Pro	Ala	Gln	Arg 95	Asp	
Pro Le	eu Ser	Ser 100	Pro	Pro	Ala	Gly	His 105	Thr	Val	Pro	Glu	Tyr 110	Arg	Asp	
Thr Va	l Ile 115	Phe	Asp	Asp	Pro	Arg 120	Leu	Val	Ser	Pro	Leu 125	Ser	Arg	Glu	,
Gly Gl 13	-	Arg	Glu	Val	Glu 135	Asp	Val	Pro	Lys	Val 140	Val	Glu	Pro	Ala	

Ser Glu Arg Glu Gly Gly Glu Arg Glu Val Glu Asp Val Pro Lys Val



•

145 5 150 155 160

Val Glu Pro Ala Ser Glu Arg Glu Gly Glu Arg Glu Val Glu Asp 165 170 175

Val Pro Lys Val Val Glu Pro Ala Ser Glu Arg Glu Gly Glu Arg 180 185 190

Glu Val Glu Asp Val Pro Lys Val Val Glu Pro Ala Ser Glu Arg Glu 195 200 205

Gly Gly Glu Arg Glu Val Glu Asp Val Pro Lys Val Val Glu Pro Ala 210 215 220

Ser Glu Arg Glu Gly Gly Glu Arg Glu Val Glu Asp Val Pro Lys Val 225 230 235 240

Val Glu Pro Ala Ser Glu Arg Glu Gly Glu Arg Glu Val Ala Ser 245 250 255

Gln His Thr Lys Gln Pro Ser His Ser Val Ser Asn Ser Ala Pro Asn
260 265 270

Gln Phe Arg Asn Pro Glu Gly Glu Leu Pro Phe Thr Leu Pro Asp Leu 275 280 285

Ser Glu Ser Glu Ile Val Val Pro Glu Glu Gln Lys Gly Arg Ala His 290 295 300

Pro Gln Val Ile Pro Glu Gly Ala Pro Arg Gly Leu Gln Pro Gly Glu 305 310 315 320

Tyr Tyr Val Gln Ile Ala Val Phe His Asp Ala Ile Gln Val Gln Ser 325 330 335

Ile Val His Arg Tyr Gly Val Glu Tyr Pro Ile Ala Val Glu Gln Asp 340 345 350

Ile His Glu Gly Lys Val Arg Phe Thr Val Cys Val Gly Pro Val Gln 355 360 365

Lys Asp Glu Arg Gly Ala Val Leu Glu Asn Phe Gln Arg Phe Gly Phe 370 375 380

Lys Asp Ala Phe Leu Lys Lys Ala Arg 385 390